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Microbiota intestinal y su relación con la obesidad en adultos: artículo de revisión

Gut microbiota and its relationship with obesity in adults: literature review

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Palabras claves: microbiota intestinal, obesidad, adultos, disbiosis, sobrepeso.

Resumen

Introducción: el microbiota intestinal ha emergido como un componente crucial para el mantenimiento de la salud humana, desempeñando roles fundamentales en la digestión, metabolismo, inmunidad, la regulación del estado nutricional y homeostasis energética. Sin embargo, la disbiosis (alteración del equilibrio del microbiota) puede causar obesidad, mediante mecanismos inflamatorios, aumento de la permeabilidad intestinal y cambios en el apetito. **Objetivo**: determinar la relación entre la alteración del microbiota intestinal y la obesidad en adultos. **Metodología:** el diseño de investigación es de tipo documental, exploratorio y descriptivo. Se realizó una revisión sistémica de los últimos 5 años de la literatura existente en bases de datos electrónicas como *Scopus, PubMed, Science direct, Web of Science*, y Google académico. Se aplicaron criterios de inclusión y exclusión. **Resultados:** aunque no se puede afirmar que el microbiota intestinal sea la causante directa de la obesidad en adultos, si existe una relación compleja y bidireccional entre los ambos. La disbiosis intestinal puede influir en el desarrollo de la obesidad, y esta a su vez puede modificar el microbiota intestinal. Los mecanismos principales son alteración en el metabolismo energético, proceso inflamatorios y regulación del apetito. **Conclusión:** la obesidad es una enfermedad metabólica crónica con múltiples factores causantes y el microbiota intestinal es solo uno de ellos. La alteración del microbiota intestinal está relacionada con la obesidad en adultos por lo que se debe manejar de manera integral, lo que incluye modificación en el estilo de vida y en ocasiones tratamiento médico. **Área de estudio general:** Medicina. **Área de estudio específica:** Microbiología. **Tipo de estudio**: Artículo de Revisión.

Keywords: Intestinal microbiota, obesity, adults, dysbiosis, overweight.

Abstract

Introduction: the intestinal microbiota has emerged as a crucial component for the maintenance of human health, playing fundamental roles in digestion, metabolism, immunity, the regulation of nutritional status and energy homeostasis. However, dysbiosis (alteration of the microbiota balance) can cause obesity, through inflammatory mechanisms, increased intestinal permeability and changes in appetite. Objective: determine the relationship between alterations in the intestinal microbiota and obesity in adults. Methodology: the research design is documentary, exploratory and descriptive. A systematic review of the last 5 years of the existing literature was conducted in electronic databases such as Scopus, PubMed, Science direct, Web of Science and Google academic. Inclusion and exclusion criteria will be applied. Results: although it cannot be stated that the intestinal microbiota is the direct cause of obesity in adults, there is a complex and bidirectional relationship between the two. Intestinal dysbiosis can influence the development of obesity, and this in turn can modify the intestinal microbiota. The main mechanisms are alterations in energy metabolism, inflammatory process, and appetite regulation. Conclusion: obesity is a chronic metabolic disease with multiple causative factors and the intestinal microbiota is only one of them. Alterations in the intestinal microbiota are related to obesity in adults, so they must be managed comprehensively, which includes lifestyle modification and sometimes medical treatment.

Introduction

The human gut microbiota, comprising trillions of microbes, plays a key role in diverse physiological functions including metabolism and immune regulation. Current research has revealed the close relationship between microbiota composition and obesity in adults. Dysbiosis characterized by alterations in microbial diversity and abundance has been implicated in the development and progression of obesity. (1) There are changes in the composition of the gut microbiota, such as a decrease in beneficial bacteria such as Bacteroidetes and an increase in potentially harmful taxa such as Firmicutes, in obese individuals compared to their lean counterparts. These alterations are related to metabolic alterations, including increased energy acquisition from the diet, increased adipogenesis, and inflammation, which contribute to weight gain and adiposity. It should be noted that dysbiotic microbiota can modify the integrity of the intestinal barrier, leading to the translocation of microbial products and triggering low-grade inflammation, which characterizes obesity. On the other hand, actions targeting the gut microbiota, such as probiotics, prebiotics, and dietary change, have been encouraging in improving obesity-related metabolic dysfunction. Modulating gut microbiota composition through these interventions can improve metabolic parameters, including insulin sensitivity and adiposity, highlighting the potential of microbiota-targeted therapies to combat obesity. However, further research is warranted to elucidate the underlying mechanisms governing the microbiota-obesity axis and optimize microbiota-based interventions for the effective treatment of obesity in adults (2).

The global prevalence of obesity has reached alarming proportions, representing a major public health problem with profound implications for morbidity, mortality, and healthcare expenditure. Obesity, characterized by excessive adiposity, is a multifactorial disorder influenced by genetic, environmental, and behavioral factors. While dietary habits and sedentary lifestyles clearly contribute to obesity, emerging evidence suggests that the gut microbiota, the diverse microbial community residing in the gastrointestinal tract, plays a crucial role in the development and pathogenesis of obesity in adults (1).

The human gut microbiota is a complex ecosystem comprising trillions of microorganisms, including bacteria, archaea, fungi, viruses, and protists, which together exert a wide range of metabolic, immunological, and physiological functions (3). Recent advances in high-throughput sequencing technologies have facilitated the comprehensive characterization of the gut microbiota, allowing researchers to explore its intricate relationship with host health and disease. Dysbiosis, defined as an imbalance in microbial composition and function, has been implicated in the pathogenesis of various metabolic disorders, including obesity, insulin resistance, and type 2 diabetes mellitus (5).

Numerous studies have documented alterations in the gut microbiota composition of individuals with obesity compared to their lean counterparts. Specifically, obesity is associated with a reduction in microbial diversity and changes in the relative abundance of specific taxa. One of the most consistent findings is an increase in the ratio of Firmicutes to Bacteroidetes, which has been proposed to enhance energy acquisition from the diet, promoting adiposity and weight gain. Furthermore, dysbiotic microbiota may contribute to low-grade inflammation, a hallmark of obesity, by producing proinflammatory metabolites and activating immune pathways (5).

Mechanistically, the gut microbiota influences host metabolism through several pathways, including modulating dietary energy extraction, regulating adipose tissue deposition and inflammation, and modulating gut barrier integrity and permeability. Short-chain fatty acids (SCFAs), microbial metabolites produced through the fermentation of dietary fibers, have emerged as key mediators of microbiota-host interaction, exerting beneficial effects on metabolic health by promoting satiety, improving insulin sensitivity, and modulating immune function (3).

In addition to its role in obesity pathogenesis, the gut microbiota represents a promising target for therapeutic intervention in the treatment of obesity and related metabolic disorders. Strategies aimed at modulating gut microbiota composition and function, such as probiotics, prebiotics, dietary modifications, and fecal microbiota transplantation

(FMT), have shown promise in improving metabolic parameters and reducing adiposity in both preclinical and clinical studies (6).

Despite significant advances in elucidating the role of the gut microbiota in obesity, several key questions remain unanswered. Further research is needed to unravel the complex interactions between the gut microbiota and host metabolism, identify microbial biomarkers of obesity risk and progression, and optimize microbiota-based therapeutic approaches for the treatment of obesity in adults (1). A deeper understanding of the microbiota-obesity axis has the potential to revolutionize obesity prevention and treatment strategies, offering new hope in the battle against this global epidemic.

Methodology

This being a review article, a documentary research design was used, characterized by a qualitative approach, being an exploratory descriptive, applied research. The research method was based on the systemic review of the existing literature. For the search strategy, the literature research was carried out in electronic databases such as Scopus, PubMed, Science Direct, Web of Science, Google Scholar. Using keywords and search terms such as "intestinal microbiota", "microbiome", "gut microbiome", "obesity", "adults", "adults", applying combinations with the Boolean operator "AND", "OR". During the development, studies were selected by their title and summary reading to discard studies that are not relevant to this research, in the selected texts a complete reading was done to verify the relevance of their information. Data was obtained from studies depending on the author, year of publication, study design, sample size of the studies evaluated. Taking into account several inclusion and exclusion criteria explained in Table 1, necessary for the completion of this review article.

Table 1. Inclusion and exclusion criteria

Inclusion criteria	Exclusion criteria
Studies evaluating intestinal microbiota and obesity	Studies that do not provide data on intestinal microbiota and obesity.
Research with human and adult participants	Studies that provide data on the intestinal microbiota in children.
Articles published maximum 5 years ago	Studies carried out on animals.
Articles published in English, Portuguese and Spanish	

The human gut microbiota, a diverse community of microorganisms residing in the gastrointestinal tract, has emerged as a key player in the pathogenesis of obesity. Numerous studies have documented associations between alterations in gut microbial composition and obesity in adults. Understanding the dynamic relationship between gut microbiota and obesity holds promise for the development of novel therapeutic strategies aimed at curbing the global obesity epidemic. In this literature review, we provide a comprehensive overview of the current perception of the microbiota-obesity axis, focusing on microbial dysbiosis, the mechanisms underlying microbial influences on host metabolism, and potential therapeutic interventions targeting the gut microbiota. Studies conducted demonstrate the diverse composition of the microbiota by comparing obese and lean individuals. In which it is shown that obese individuals have a microbiota composed mostly of Firmicutes and in a lesser proportion we find Bacteroidetes (7).

Dysbiosis, characterized by alterations in gut microbial composition and function, has been consistently observed in obese individuals in contrast to their lean counterparts. One of the most significant findings is an increase in the proportion of Firmicutes and Bacteroidetes, in relation to increased dietary energy uptake and adiposity. Furthermore, reduced microbial diversity and changes in the relative abundance of specific taxa, such as reduced levels of butyrate-producing bacteria and increased abundance of opportunistic pathogens, have been reported in obese individuals. These alterations in microbial composition are thought to contribute to metabolic disturbances, including insulin resistance, inflammation, and dysregulation of lipid metabolism, ultimately promoting weight gain and obesity (8).

The gut microbiota impacts host metabolism through a variety of mechanisms, including regulation of dietary energy extraction, adjustment of deposition, inflammation of adipose tissue, and control of intestinal barrier integrity and permeability. Short-chain fatty acids (SCFAs), microbial metabolites produced by the fermentation of dietary fibers, play a key role in mediating the microbiota-host relationship. SCFAs, especially butyrate, acetate, and propionate, function as an energy source for colonic epithelial cells, modulate intestinal barrier function, and have anti-inflammatory effects. Furthermore, gut microbiota-derived metabolites, such as secondary bile acids, trimethylamine N-oxide (TMAO), and lipopolysaccharides (LPS), can impact systemic metabolism and contribute to obesity-related metabolic dysfunction (2).

In terms of fat storage regulation, certain gut bacteria can impact fatty acid absorption and fat storage in adipose tissue. For example, the microbiota in obese individuals has been shown to have the ability to extract more energy from the diet, which ultimately leads to excess fat storage. (1) Systemic and local inflammation occurs in the case of dysbiosis, i.e. an imbalance of the microbiota, intestinal permeability will increase, allowing the passage of lipopolysaccharides and other pro-inflammatory molecules into the systemic circulation. This process, in turn, can lead to long-term low-grade inflammation, which is often associated with insulin resistance and weight gain (9). Another area under the influence of the microbiota is the production and release of intestinal hormones PYY and GLP-1, which control appetite and satiety. A normal microbiota also improves insulin sensitivity and satiety, a dysbiosis can contribute to hyperphagia and insulin resistance (5).

Controlling the metabolism of bile acids, the intestinal microbiota is responsible for transforming bile acids from primary to secondary, so they are involved in the regulation of glucose and lipid metabolism, their stimulation can lead to the accumulation of fat and generate insulin resistance (5).

Among the therapeutic interventions guided to the intestinal microbiota, it is observed that the adjustment of the structure and function of the intestinal microbiota represents a promising perspective for the approach to obesity and associated metabolic disorders. (10) Probiotics, being live microorganisms with an amalgam of health benefits that contribute to the improvement of intestinal health and metabolism, and prebiotics, non-digestible fibers that selectively promote the growth of beneficial bacteria, have shown promising changes to improve metabolic parameters and reduce adiposity in animal and human studies. In addition, dietary interventions, such as the consumption of fiber-rich foods and fermented products, the reduction of fat and sugar, can promote a favorable profile of the intestinal microbiota and mitigate the risk of obesity. Fecal microbiota transplantation (FMT), the transfer of fecal microbiota from healthy donors to recipients has emerged as a therapeutic option to restore microbial diversity and function in people with obesity and metabolic syndrome (11).

Results

The intestinal microbiota of a healthy adult is composed of intestinal bacteria, 90% of which are Bacteroidetes and Firmicutes, 10% of which are made up of Proteobacteria, Actinobacteria, Verrucomicrobia, Fusobacteria and a few species of Archaea. In viral representation, the intestinal microbiota is dominated by bacteriophages, performing their function of horizontal gene transfer and monitoring the reproduction of dominant species. Part of the intestinal microbiota are yeasts with less than 20 species, but their cell size is much larger than that of bacteria (1).

The microbiota is different in each section of the digestive system, the same strains can be found, but in different proportions. Changes in the microbiota have been observed in the same individual due to factors such as drugs, diet, the duration of passage of fecal content through the intestine, trips made, but the changes observed from one individual to another are much greater, although the changes will become noticeable, the microbiota maintains its typical pattern for which it is called enterotype in this case the diet will be the greatest conditioning factor (2).

The enterotypes are going to be classified into:

- Enterotype 1: Characterized by Bacteroides (2).
- Enterotype 2: prevotella predominates (2).
- Enterotype 3: We found ruminococcus or bifidobacterium (2).

One of the favorable characteristics of the microbiota is its power to return to its normal state, that is, when imbalances occur such as in diarrhea or antibiotic treatments where the microbiota is affected (1).

As a person ages, microbial loss and notable changes in some microorganisms belonging to the microbiota are observed, due to immune dysfunction, causing inflammatory processes. A decrease in microorganisms such as bifidobacteria and faecalibacterium prausnitzii, which have anti-inflammatory capacity, can be observed. This deterioration can be avoided by oral supplementation with some of these microorganisms such as Akkermansia muciniphila.

To maintain a stable intestinal microbiota, a correct microbe-microbe interaction is required. The representation of the microbiota in a healthy individual is shown in Figure 1. The intestinal microbiota consists of microorganisms with more than 1000 species of bacteria, as well as viruses, fungi, eukaryotes, and archaea, which together add up to approximately 100 billion microorganisms (11).

The microbiota will fulfill different functions in the body such as:

1. Nutrient absorption
2. Digestion
3. Defense against pathogenic infections
4. Maturation of the immune system
5. Preservation of intestinal barrier function
6. Preservation of intestinal selective permeability (11).

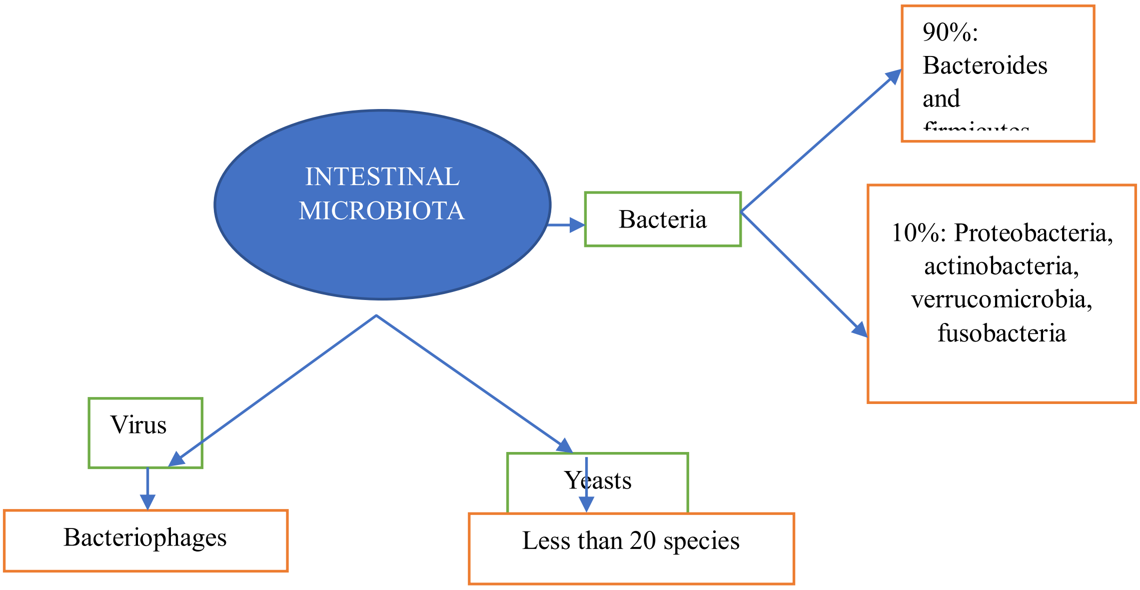

Figure 1. Representation of the normal intestinal microbiota

Within the diversity of the microbiota in relation to obesity, it can be seen that the ecosystem of our intestine dominated by the intestinal microbiota suffers from dysbiosis in people who are obese. When talking about the intestinal flora of an adult, it must be remembered that this is influenced by the type of delivery, whether vaginal or cesarean, through which the individual was born, in addition to its dependence on their biology, lifestyle, environment and health system in which the individual develops.

Table 2. Factors that depend on the individual's health and microbiota

Biology	1. Genetics 2. Development 3. Aging
Lifestyle	1. Feeding 2. Exercise 3. Use of drugs 4. Toxic practices
Environment (external factors)	**1.** Physicists **2.** Chemicals **3.** Biologicals **4.** Psychosocial **5.** Sociocultural
Healthcare system	1. Use of services 2. Effectiveness 3. Efficiency

Fountain: Data taken from Alvarez J., Intestinal microbiota and health, Elsevier gastroenterology and hepatology.

The microbiota plays an important role in the digestion and absorption of nutrients, collaborating in the fermentation of undigested carbohydrates, the synthesis of vitamins and the metabolization of bioactive compounds. In some cases, certain intestinal bacteria, such as those of the genus Bacteroides and Bifidobacterium, are considered capable of breaking down dietary fiber into short-chain fatty acids, which have the capacity to be absorbed and used as an energy source by the host. On the other hand, the intestinal microbiota helps the absorption of minerals such as calcium, iron and magnesium, through a process of regulation of intestinal acidity and the expression of nutrient transporters in the intestinal mucosa (3).

The microbiota in relation to nutrition-related diseases Alterations in the composition and function of the intestinal microbiota have been associated with a number of nutrition-related disorders, including obesity, type 2 diabetes, cardiovascular disease and mood disorders. It has been suggested that intestinal dysbiosis, characterized by an imbalance in the microbiota, may contribute to the development and progression of these diseases, either through chronic inflammation, insulin resistance or the production of toxic metabolites. In an article carried out at the University of Virginia in 2019, on the management of metabolic syndrome, obesity is considered of great importance as a chronic and progressive disease since it can be the protagonist and pathway for other diseases such as diabetes and insulin resistance, institutions such as the International Diabetes Federation consider the presence of central obesity to classify metabolic syndrome, without taking into account other pathologies belonging to the metabolic syndrome, obesity in constant evolution is considered an aggravating factor in the prevalence of metabolic syndrome by race and ethnicity, considering one of the best strategies for preventing metabolic syndrome the prevention and treatment of obesity, considering the difficulty of losing weight it has been seen that the best option would be to prevent obesity (4).

Regarding the changes in the microbiota, a study carried out in 2022 shows the characteristics of the intestinal microbiota in people with an ideal weight, overweight and obesity, analyzing fecal samples from 4893 people of which 2236 people have a normal weight, this being the control sample, 1152 samples from overweight people, and 894 samples from people with obesity. Finding significant differences in the intestinal microbiota between the control group and the group with obesity, noting a decrease in the proportion of bacteroidetes and firmicutes in people with obesity, evaluating this as a biomarker of dysbiosis present in simple obesity. In addition, a decrease in Christensenellaceae, Ruminococcus-1, Akkermansia, Lachnospiraceae is observed in the simple obesity group, being associated with the increase in the percentage of body fat to*Ruminococcus gnavus.*The insufficiency ofAkkermansia leads to high energy extraction from food, thus causing obesity. Akkermansia has been seen as a therapeutic and prevention option for obesity (5).

Measures such as bariatric surgery, weight reduction and restoration of bacterial dysbiosis are used in the treatment of obesity (1). In a 2020 double-blind placebo-controlled pilot study of fecal microbiota transplantation to improve metabolism in obesity, the safety of capsule fecal transplantation as a treatment for obesity was observed. Oral fecal microbiome transplantation alone is insufficient in the treatment and prevention of obesity (12). Among the effective treatments, a randomized controlled trial on avocado consumption was observed to alter the abundance of gastrointestinal bacteria and the concentrations of microbial metabolites among overweight and obese adults, resulting in a significant increase in the intestinal microbiota in patients who consumed avocado daily, as well as an improvement in the lipid profile, reduction in adiposity and an increase in the concentration of metabolites derived from microbiosis in adults who are overweight and obese, thus providing very important information on the impact of avocado consumption on the intestinal microbiota and its collaboration in dietary treatments to control obesity (13).

In a randomized trial published in 2022, caloric restriction is mentioned to improve the metabolic status regardless of the composition of the intestinal microbiota. It is observed that there are no significant changes in the intestinal microbiota in obese and overweight patients induced to caloric restriction, however, an improvement in the metabolic status of the patients is observed (14).

Conclusions

- The diversity of the intestinal microbiota is closely related to obesity, its development and progression. Dysbiosis, in which a decrease in bacterial diversity is observed and the modifications present in the proportion of various bacterial strains can contribute to weight gain and lead to obesity. There are specific studies that support the role of the microbiota in the control of energy metabolism and inflammation, these two points being very important in reaching obesity. It was observed that diet becomes a key factor in the modulation of the intestinal microbiota, thus being the key to the prevention and treatment of obesity. A diet low in saturated fats, refined sugars and high in fiber is an important factor in increasing microbial diversity, thereby preventing obesity and helping with weight loss. The importance of using prebiotics, probiotics and fecal microbiota transplantation is also observed, as viable and very promising options for treating obesity. Controlled clinical trials and longitudinal studies are considered necessary to demonstrate the cause-effect relationship between microbiota and obesity in adults, as well as to evaluate the long-term consistency of treatments and interventions aimed at preventing and treating obesity through microbiota balance.

Conflict of interest

The author declares that there is no conflict of interest with this study.

Authors' contribution

The sole author Franklin Hernán Cashabamba Padilla was responsible for all activities including conceptualization, methodology, software, validation, investigation, resources, data curation, writing, visualization, supervision, and funding of the project. Franklin Hernán Cashabamba Padilla declares that he performed all of the above tasks independently.

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